AMENDMENTS TO THE SPECIFICATION

Please delete the existing title of this application and insert –CD27 CODING SEQUENCE—therefor.

Please replace the paragraph on page 13, lines 16-22, with the following amended paragraph:

Figures 2A-2B. Nucleotide sequence of the CD2cDNA insert (SEQ ID NO:2)

Nucleotide numbering is given in parentheses at right, amino acid numbering, left. Locations of the potential sites for addition of asparagine-linked carbohydrate (CHO) are shown, as well as the predicted transmembrane (TM) sequence. The amino acid sequence is numbered from the projected cleavage site of the secretory signal sequence. See also SEQ ID NO:3 for the amino acid sequence.

Please replace the paragraph on page 14, lines 1-9, with the following amended paragraph:

Figures 4A-4B. Nucleotide sequence and corresponding amino acid sequence of the LFA-3 antigen (SEQ ID NO:4 and SEQ ID NO:5)

WOP cells transfected with a clone encoding the LFA-3 antigen were detected by indirect immunofluorescence, amplified and sequenced. Fig. 4A shows the 874 base pair insert containing an open reading frame of 237 residues originating at a methionine codon, and terminating in a series of hydrophobic residues. Hydrophobic and hydrophilic regions within this open reading frame are shown in Fig. 4B.

Please replace the paragraph on page 14, lines 22-28, with the following amended paragraph:

Figures 7A-7B. Nucleotide sequence of the CD28 cDNA (SEQ ID NO:7)

Nucleotide numbering is given in parentheses at right, amino acid numbering, center and left. Location of the potential sites for addition of asparagine-linked carbohydrate (CHO) are shown, as well as the predicted transmembrane (TM) sequence. The amino acid sequence is numbered from the projected cleavage site of the secretory signal sequence.

See also SEQ ID NO:8 for the CD28 amino acid sequence.

Please replace the paragraph on page 15, lines 12-18, with the following amended paragraph:

Figures ~~10A-10C~~ 10A-1-10A-2 and 10B. Sequence of the CD20.4 cDNA (SEQ ID NO:11) Figures ~~10A-10B~~ 10A-1-10A-2. The sites of potential N-linked glycosylation are denoted by the symbol -CHO-; the hydrophobic regions are underscored. See also SEQ ID NO:12 for theCD20.4 amino acid sequence. The site of the poly(A)$^+$ tail in clone CD20.6 is denoted by an asterisk.
~~Figure 10C.~~ Figure 10B. Hydrophobicity profile of the amino acid sequence in Figures ~~10A-10B.~~ 10A-1-10A-2 . See also SEQ ID NO:12.

Please replace the fourth paragraph at page 15, lines19-29 with the following amended paragraph:

Figures 11A-11C. Sequence of ICAM-1 (SEQ ID NO:13)

Complete nucleotide sequence of ICAM-1 cDNA insert and predicted protein sequence (SEQ ID NO:14). Nucleotide numbering is at left, amino acid numbering, center. The RGE motif at position 128 is underlined, the potential N-linked glycosylation sites are indicated by -CHO- and the transmembrane domain by -TM-. The amino acid sequence is numbered from the projected cleavage site of the signal peptide. Sequencing was by dideoxy-chain termination (Sanger, F., et al., Proc. Natl. Acad. Sci. USA 74:5463-5467 (1977)), using a combination of subclones, and specific oligonucleotides.

Please replace the paragraph on page 25, lines 9-16, with the following amended paragraph:

Even more preferred for the purposes of the present invention are the expression

vectors designated piH3, piH3M, and CDM8, deposited at the American Type Culture Collection (ATCC), ~~12301 Parklawn Drive, Rockville, MD 20852~~ 10801 University Boulevard, Manassas, VA 20110-2209. piH3 was deposited at the ATCC on February 24, 1988, and has accession number ATCC 67634. piH3M was deposited at the ATCC on February 24, 1988, and has accession number ATCC 67633. CDM8 was deposited at the ATCC on February 24, 1988, and has accession number ATCC 67635.

At page 29, please amend the title of the table as follows:

Table 1. (SEQ ID NO:20 and SEQ ID NO:21).

At page 31, please amend the title of the table as follows:

Table 2. (SEQ ID NO:22 and SEQ ID NO:23).

At page 32, please amend the title of the table as follows:

Table 3. (SEQ ID NO:24 and SEQ ID NO:25).

At page 33, please amend the title of the table as follows:

Table 4. (SEQ ID NO:26 and SEQ ID NO:27).

At page 95, lines 4-16, please rewrite as follows:

The nucleotide sequence of the cDNA was determined by dideoxynucleotide chain termination as described, supra. The sequence of 1203 residues and the deduced amino acid sequence appear in Table 5. See also SEQ ID NO:28 and 29. The initiation methionine is indicated by the number 1 above the initiator codon. The deduced CD27 polypeptide demonstrates the typical features of a type I integral

membrane protein. It begins with a twenty amino acid hydrophobic region consistent with a secretory signal sequence. This hydrophobic region is followed by a 171 residue extracellular domain, a 20 residue hydrophobic membrane spanning domain (doubly underlined) and a 49 amino acid cytoplasmic domain beginning with a positively charged stop transfer sequence. There is no poly (A) tail.

Please replace page 96 with the amended page 96 attached hereto. Amino acid 34 has been changed from R to A for consistency with the relevant codon in the coding sequence. The title has been amended to add reference to

At page 105, please amend the title of the table as follows:

Table 7. (SEQ ID NO:31 and SEQ ID NO:32).

At page 109, please amend the title of the table as follows:

Table 8. (SEQ ID NO:33 and SEQ ID NO:34).

At page 115, please amend the title of the table as follows:

Table 9. (SEQ ID NO:35 and SEQ ID NO:36).